ABSTRACT

Background:

C.auris with a highly divergent genome is an emerging etiologic agent of fungemia. *C.auris* isolated in India was found to be resistant to fluconazole and genotypically distinct from isolates from South Korea and Japan. There is an urgent need for accurate fungal screening methods such as PCR to ensure proper management of fungemia. *C.auris* fungemia is associated with a high mortality rate (66%).*C.auris* has a highly divergent genome.

Aim and objective:

To identify the presence of *C.auris* in the saliva of immunocompromised patients, denture wearers and normal individuals by quantitative real time polymerase chain reactions(RT- PCR/q PCR)

Material and methods:

Unstimulated saliva was collected from 10 HIV patients, 10 denture wearers and 10 normal individuals. In order to identify the quantitative presence of C. auris, 10ng of total DNA isolated from the saliva of HIV patients, denture wearers or normal control subjects was subjected to real time PCR

Results:

The results were obtained in amplification curve. Samples with higher concentration of *C.auris* specific signal showed early Ct values, while samples with lower concentration of *C.auris* specific signal showed delayed Ct values. Saliva samples of denture wearers showed higher content of high copy numbers of *C.auris*.

Conclusion:

Molecular methods are accurate and rapid method of identification of *C.auris*. Real Time Polymerase Chain Reaction (RT-PCR) proved to be highly specific and sensitive method of identification of the rare nosocomial pathogen *C.auris*.

Keywords: Candida auris, RT-PCR, Cycle Threshold